

ABSTRACT

Disclosed are a number of methods that can be used in a variety of embodiments, including, creation of a nucleic acid terminated at one or more selected bases, sequence analysis of nucleic acids, mapping of sequence motifs within a nucleic acid, positional mapping of nucleic acid clones, and analysis of telomeric regions. The methods utilize double-stranded templates, and in most aspects involve a strand replacement reaction initiated at one or more random or specific locations created in a nucleic acid molecule, and in certain aspects utilizing an oligonucleotide primer.